SEQUENCE LISTING

<110> Wang, Xiangbin
Huang, Hualiang
Zhao, Baofeng
Zhao, Qi
Piao, Jinhua
Lin, Qing

<120> A GENETIC ENGINEERING RECOMBINANT ANTI-CEA, ANTI-CD3 AND ANTI-CD28 SINGLE-CHAIN TRI-SPECIFIC ANTIBODY

<130> 11774-006-999 (I040179)

<150> PCT/CN2005/000408
<151> 2005-03-29

<150> CN 200410032158.3
<151> 2004-04-01

<160> 58

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 251
<212> PRT
<213> Murine

<220>
<223> murine anti-CEA single chain fragment of variable region contained in CEA-scTsAb

<400> 1

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met	Lys	Pro	Gly	Ala
1				5				10						15	
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Asp	Tyr
			20					25					30		
Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Glu	Ile	Leu	Pro	Gly	Ser	Gly	Arg	Thr	Asp	Tyr	Asn	Glu	Arg	Phe
	50					55					60				
Lys	Gly	Lys	Ala	Thr	Phe	Thr	Gly	Asp	Val	Ser	Ser	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Lys	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Thr	Gly	Thr	Thr	Pro	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ala	Thr	Ser	Thr	Pro	Ser	His	Asn	Ser	His	Gln	Val	Pro
		115					120					125			
Ser	Ala	Gly	Gly	Pro	Thr	Ala	Asn	Ser	Gly	Ser	Arg	Asp	Ile	Val	Leu
	130					135					140				
Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr
145					150					155					160
Ile	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Thr	Ser	Ser	Tyr	Thr	Tyr
				165					170					175	
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile
			180					185					190		
Lys	Tyr	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly
		195					200					205			

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
    210                 215                 220
Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp Glu Ile Pro Arg
225                 230                 235                 240
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                245                 250
```

<210> 2
<211> 250
<212> PRT
<213> Murine

<220>
<223> murine anti-CEA single chain fragment of variable region contained in CEA-scTsAb

<400> 2

```
Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln
    130                 135                 140
Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
145                 150                 155                 160
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp
                165                 170                 175
Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr
            180                 185                 190
Ser Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser
        195                 200                 205
Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile
    210                 215                 220
Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala
225                 230                 235                 240
Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala
                245                 250
```

<210> 3
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-scTsAb sequence

<400> 3

atgggtctcg agcaggtgca gctgcagcag agcggtgcgg aactgatgaa accgggcgcg 60
agcgtgaaaa tcagctgcaa agcgaccggc tataccttca gcgattattg gatcgaatgg 120
gtgaaacagc gtccgggtca cggcctggaa tggatcggtg aaatcctgcc gggcagcggc 180
cgtaccgact acaacgaacg tttcaaaggc aaagcgacct tcaccggcga cgtttctagc 240
aacaccgcgt atatgaaact gtctagcctg accagcgaag atagcgcggt gtattactgc 300
gcgaccggca ccaccccgtt cggttactgg ggtcagggca ccctggttac cgtttccgcg 360
actagtaccc cgagccataa cagccatcag gtgccgagcg cgggcggccc gaccgcgaac 420
agcggctcta gagacatcgt gctgacccag agcccggcga gcctggcggt gtctctgggt 480
cagcgtgcga ccatctcctg ccgtgcttcc cagtccgttt ccacctcctc ctacacctac 540
atgcactggt atcagcagaa accgggtcag ccgccgaaac tgctgatcaa atatgcgagc 600
aacctggaat ctggtgtgcc ggcgcgtttc agcggttctg gcagcggcac cgacttcacc 660
ctgaacatcc acccggtgga agaagaagat accgcgtatt actattgcca gcactcttgg 720
gaaatcccgc gtaccttcgg tggcggcacc aaactggaaa tcaaagaatt caacagcacg 780
taccgggttg taagcgtcct caccgtactg caccaggact ggctgaatgg caaggaatac 840
aaatgcaaga gtactgaggt gaagctggtg gagtctggac ctgagctggt gaagcctgga 900
gcttcaatga agatatcctg caaggcttct ggttactcat tcactggcta caccatgaac 960
tgggtgaagc agagtcatgg aaagaacctt gagtggatgg gacttattaa tccttacaaa 1020
ggtgttagta cctacaacca gaagttcaag gacaaggcca cattaactgt agacaagtca 1080
tccagcacag cctacatgga actcctcagt ctgacatctg aggactctgc agtctattac 1140
tgtgcaagat cggggtacta cggtgatagt gactggtact tcgatgtctg gggcgcagga 1200
acctcagtca ctgtctcctc aactagtggt ggtggtggtt ctggtggtgg tggttctggt 1260
ggtggtggtt cttctagaga catccagatg acccagacca catcctccct gtctgcctct 1320
ctgggagaca gagtcaccat cagttgcagg gcaagtcagg acattagaaa ttatttaaac 1380
tggtatcaac agaaaccaga tggaactgtt aaactcctga tctactacac atcaagatta 1440
cactcaggag tcccatcaaa gttcagtggc agtgggtctg gaacagatta ttctctcacc 1500
attagcaacc tggagcaaga ggatattgcc acttactttt gccaacaggg taatacgctt 1560
ccgtggacgt tcgctggagg caccaaactg gaactgaagc gcgctgtcga cttccagaat 1620
gcgctgctgg ttcgttacac caagaaagta ccccaagtgt caactccaac tcctgtagag 1680
gtctcacata tgcaggtaca gctacaggaa tctggtccgg gtctggtaaa accgtctcag 1740
accctgtctc tgacctgtac cgtatctggt ttctctctgt ctgactatgg tgttcattgg 1800
gtacgtcagc cgccaggtaa aggtctggaa tgtctgggtg taatatgggg tggaggcacg 1860
aattataatt cggctctcat gtccagacgt gtaacctctt ccgacgatac ctctaaaaat 1920
cagttctctc tgaaactgtc ttccgtagac accgctgtat actattgtgc tcgttcctat 1980
tactattcta tggactactg gggtcagggc accctggtaa ccgtatcttc cggtaccgaa 2040
caaaaactca tctcagaaga ggatctgaat ggggccgcac atcatcatca ccatcacgag 2100
caa 2103

<210> 4
<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-scTsAb sequence

<400> 4

Met	Gly	Leu	Glu	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met
1				5				10					15		
Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr
			20					25					30		
Phe	Ser	Asp	Tyr	Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly
		35					40					45			
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Gly	Arg	Thr	Asp	Tyr
	50					55					60				
Asn	Glu	Arg	Phe	Lys	Gly	Lys	Ala	Thr	Phe	Thr	Gly	Asp	Val	Ser	Ser
65					70					75					80
Asn	Thr	Ala	Tyr	Met	Lys	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala
				85					90					95	
Val	Tyr	Tyr	Cys	Ala	Thr	Gly	Thr	Thr	Pro	Phe	Gly	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Thr	Ser	Thr	Pro	Ser	His	Asn	Ser

```
        115                 120                 125
His Gln Val Pro Ser Ala Gly Gly Pro Thr Ala Asn Ser Gly Ser Arg
    130                 135                 140
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
145                 150                 155                 160
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
                165                 170                 175
Ser Tyr Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
            180                 185                 190
Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
        195                 200                 205
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
    210                 215                 220
Pro Val Glu Glu Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp
225                 230                 235                 240
Glu Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu
                245                 250                 255
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            260                 265                 270
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Ser Thr Glu Val Lys
        275                 280                 285
Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys
    290                 295                 300
Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
305                 310                 315                 320
Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile
                325                 330                 335
Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys
            340                 345                 350
Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu
        355                 360                 365
Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser
    370                 375                 380
Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly
385                 390                 395                 400
Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly Ser Gly Gly
                405                 410                 415
Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln Met Thr Gln
            420                 425                 430
Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser
        435                 440                 445
Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln
    450                 455                 460
Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu
465                 470                 475                 480
His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp
                485                 490                 495
Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr
            500                 505                 510
Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr
        515                 520                 525
Lys Leu Glu Leu Lys Arg Ala Val Asp Phe Gln Asn Ala Leu Leu Val
    530                 535                 540
Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Pro Val Glu
545                 550                 555                 560
Val Ser His Met Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
                565                 570                 575
Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser
            580                 585                 590
Leu Ser Asp Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly
        595                 600                 605
```

```
Leu Glu Cys Leu Gly Val Ile Trp Gly Gly Gly Thr Asn Tyr Asn Ser
    610                 615                 620
Ala Leu Met Ser Arg Arg Val Thr Ser Ser Asp Asp Thr Ser Lys Asn
625                 630                 635                 640
Gln Phe Ser Leu Lys Leu Ser Ser Val Asp Thr Ala Val Tyr Tyr Cys
                645                 650                 655
Ala Arg Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Leu
            660                 665                 670
Val Thr Val Ser Ser Gly Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp
        675                 680                 685
Leu Asn Gly Ala Ala His His His His His His Glu Gln
    690                 695                 700
```

<210> 5
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of CEA-scTsAb

<400> 5
tataccatgg gtctcgag 18

<210> 6
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of CEA-scTsAb

<400> 6
tataccatgg gtctcgagat gtacccgcgc ggtaacacta gtgaattcaa cagcacgta 59

<210> 7
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of CEA-scTsAb

<400> 7
agccagtcct ggtgcagtac ggtgaggacg cttacaaccc ggtacgtgct gttgaattc 59

<210> 8
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of CEA-scTsAb

<400> 8
ctgcaccagg actggctgaa tggcaaggaa tacaaatgca agagtacttc tagaatgta 59

<210> 9
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 9
cgaaccagca gcgcattctg gaagtcgacg ttaccgcgcg ggtacattct agaagtact 59

<210> 10
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 10
aatgcgctgc tggttcgtta caccaagaaa gtaccccaag tgtcaactcc aactcctgt 59

<210> 11
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 11
gcggtaccgt taccgcgcgg gtacatcata tgtgagacct ctacaggagt tggagttga 59

<210> 12
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 12
cgcggtaacg gtaccgcgct ggaagttgac gaaacctacg ttccgaaaga atttaacgc 59

<210> 13
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 13
tcgctagccc catccgcggg atgtcagcgt ggaaggtgaa ggtttccgcg ttaaattctt 60
tcgg 64

<210> 14
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 14
atcgagctca tgtacccgcg cggtaacgct agcgaacaaa aactcatctc agaagagga 59

<210> 15
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 15
tattgctcgt gatggtgatg atgatgtgcg gccccattca gatcctcttc tgagatgag 59

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 16
ctcgacggat ccttattgct cgtgatggtg 30

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 17
taatacgact cactataggg ga 22

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 18
gctagttatt gctcagcgg 19

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 19
tcacatatgc aggtacagct acag 24

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 20
ttcgctagcg gaagatacgg tacca 25

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 21
aagagtactg aggtgaagct ggtgg 25

<210> 22
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 22
gaagtcgaca gcgcgcttca gttccag 27

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic linker peptide linking VL and VH of
anti-CEA monoclonal antibody

<400> 23
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 24
ttcctcgagc aggttcagct 20

<210> 25
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 25
tcgcgcccgg tttcatcagt tccgcaccgc tctgctgcag ctgaacctgc tcgaggaa 58

<210> 26
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 26
actgatgaaa ccgggcgcga gcgtgaaaat cagctgcaaa gcgaccggct ataccttc 58

<210> 27
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 27
cacccattcg atccaataat cgctgaaggt atagccggtc gctt 44

<210> 28
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 28
attattggat cgaatgggtg aaacagcgtc cgggtcacgg cctggaatgg atcggtgaa 59

<210> 29
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 29
acgttcgttg tagtcggtac ggccgctgcc cggcaggatt tcaccgatcc attccagg 58

<210> 30
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 30
cgtaccgact acaacgaacg tttcaaaggc aaagcgacct tcaccggcga cgtttctagc 60

<210> 31
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 31
ttcgctggtc aggctagaca gtttcatata cgcggtgttg ctagaaacgt cgccggtgaa 60

<210> 32
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 32
tgtctagcct gaccagcgaa gatagcgcgg tgtattactg cgcgaccggc accaccccg 59

<210> 33
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 33
gctcacggtc accagggtgc cctgacccca gtaaccgaac ggggtggtgc cggtcgcgca 60

<210> 34
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 34
gcaccctggt gaccgtgagc gcgactagta ccccgagcca taacagccat caggtgccg 59

<210> 35
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 35
gtctctagag ccgctgttcg cggtcgggcc gcccgcgctc ggcacctgat ggctgttat 59

<210> 36
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 36
cgaacagcgg ctctagagac atcgtgctga cccagagccc ggcgagcctg gcggtgtc 58

<210> 37
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 37
ctgggaagca cggcaggaga tggtcgcacg ctgacccaga gacaccgcca ggctcgccgg 60

<210> 38
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 38

tctcctgccg tgcttcccag tccgtttcca cctcctccta cacctacatg cactggtat 59

<210> 39
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 39
gatcagcagt ttcggcggct gacccggttt ctgctgatac cagtgcatgt aggtgt 56

<210> 40
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 40
agccgccgaa actgctgatc aaatatgcga gcaacctgga atctggtgtg ccggcgcgt 59

<210> 41
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 41
gttcagggtg aagtcggtgc cgctgccaga accgctgaaa cgcgccggca caccagatt 59

<210> 42
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 42
gcaccgactt caccctgaac atccacccgg tggaagaaga agataccgcg tattactat 59

<210> 43
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 43
gccaccgaag gtacgcggga tttcccaaga gtgctggcaa tagtaatacg cggtatctt 59

<210> 44
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 44
tcccgcgtac cttcggtggc ggcaccaaac tggaaatcaa agaattcgcc 50

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 45
ggcgaattct ttgatttcca g 21

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 46
ggcgaattct ttgatttcca g 21

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 47
agccgccgaa actgctgatc 20

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 48
gatcagcagt ttcggcggct 20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 49
cgaacagcgg ctctagagac 20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 50
gtctctagag ccgctgttcg 20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 51
gtaccgacta caacgaacgt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic fragment for making construct of
CEA-scTsAb

<400> 52
acgttcgttg tagtcggtac 20

<210> 53
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FC linker

<400> 53
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
1 5 10 15
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

20 25

<210> 54
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> HSA linker 1

<400> 54
Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val
1 5 10 15
Ser Thr Pro Thr Pro Val Glu Val Ser
20 25

<210> 55
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> SHA linker 2

<400> 55
Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu
1 5 10 15
Thr Phe Thr Phe His Ala Asp Ile
20

<210> 56
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> cmyc tag

<400> 56
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 57
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 57
His His His His His His
1 5

<210> 58
<211> 437

<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence showing multiple cloning sites (fig 3)

<400> 58
tataccatgg gtctcgagat gtacccgcgc ggtaacacta gtgaattcaa cagcacgtac 60
cgggttgtaa gcgtcctcac cgtactgcac caggactggc tgaatggcaa ggaatacaaa 120
tgcaagagta cttctagaat gtacccgcgc ggtaacgtcg acttccagaa tgcgctgctg 180
gttcgttaca ccaagaaagt accccaagtg tcaactccaa ctcctgtaga ggtctcacat 240
atgatgtacc cgcgcggtaa cggtaccgcg ctggaagttg acgaaaccta cgttccgaaa 300
gaatttaacg cggaaacctt caccttccac gctgacatcc cgcggatggg gctagcgaac 360
aaaaactcat ctcagaagag gatctgaatg gggccgcaca tcatcatcac catcacgagc 420
aataaggatc cgtcgag 437